

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/347,748DATE: 12/29/94
TIME: 11:13:31

INPUT SET: S1679.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Kaushansky, Kenneth
6
7 (ii) TITLE OF INVENTION: Methods of Stimulating Erythropoiesis
8 Using Hematopoietic Proteins.
9
10 (iii) NUMBER OF SEQUENCES: 6
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: ZymoGenetics, Inc.
14 (B) STREET: 1201 Eastlake Avenue East
15 (C) CITY: Seattle
16 (D) STATE: WA
17 (E) COUNTRY: USA
18 (F) ZIP: 98102
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Parker, Gary E
33 (B) REGISTRATION NUMBER: 31-648
34 (C) REFERENCE/DOCKET NUMBER: 94-09C2
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 206-442-6673
38 (B) TELEFAX: 206-442-6678
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1062 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: double

RAW SEQUENCE LISTING

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47         (D) TOPOLOGY: linear
48
49     (ii) MOLECULE TYPE: cDNA
50
51
52     (ix) FEATURE:
53         (A) NAME/KEY: CDS
54         (B) LOCATION: 1..1059
55
56
57     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59     ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA      48
60     Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala
61         1             5             10             15
62
63     AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC      96
64     Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
65             20             25             30
66
67     CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC      144
68     Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
69             35             40             45
70
71     CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT      192
72     Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
73             50             55             60
74
75     GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG      240
76     Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
77         65             70             75             80
78
79     GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG      288
80     Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
81             85             90             95
82
83     GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG      336
84     Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
85             100             105             110
86
87     CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC      384
88     Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
89             115             120             125
90
91     CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT      432
92     Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp
93             130             135             140
94
95     CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG      480
96     Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
97         145             150             155             160
98
99     CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC      528

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100	Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala	
101	165 170 175	
102		
103	CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG	576
104	Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu	
105	180 185 190	
106		
107	AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT	624
108	Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr	
109	195 200 205	
110		
111	GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA	672
112	Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly	
113	210 215 220	
114		
115	TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG	720
116	Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu	
117	225 230 235 240	
118		
119	GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA	768
120	Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly	
121	245 250 255	
122		
123	ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG	816
124	Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro	
125	260 265 270	
126		
127	GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC	864
128	Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu	
129	275 280 285	
130		
131	CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT	912
132	Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr	
133	290 295 300	
134		
135	ACG CTC TTC CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC	960
136	Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu	
137	305 310 315 320	
138		
139	CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC	1008
140	His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser	
141	325 330 335	
142		
143	CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA	1056
144	Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu	
145	340 345 350	
146		
147	GGG TAA	1062
148	Gly	
149		
150		
151		
152	(2) INFORMATION FOR SEQ ID NO:2:	

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153

154

(i) SEQUENCE CHARACTERISTICS:

155

(A) LENGTH: 353 amino acids

156

(B) TYPE: amino acid

157

(D) TOPOLOGY: linear

158

159

(ii) MOLECULE TYPE: protein

160

161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

162

163 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala

164

1 5 10 15

165

166 Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val

167

20 25 30

168

169 Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser

170

35 40 45

171

172 Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala

173

50 55 60

174

175 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys

176

65 70 75 80

177

178 Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met

179

85 90 95

180

181 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly

182

100 105 110

183

184 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu

185

115 120 125

186

187 Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp

188

130 135 140

189

190 Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val

191

145 150 155 160

192

193 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala

194

165 170 175

195

196 Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu

197

180 185 190

198

199 Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr

200

195 200 205

201

202 Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly

203

210 215 220

204

205 Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu

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206      225      230      235      240
207
208  Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly
209      245      250      255
210
211  Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro
212      260      265      270
213
214  Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu
215      275      280      285
216
217  Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr
218      290      295      300
219
220  Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
221  305      310      315      320
222
223  His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
224      325      330      335
225
226  Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu
227      340      345      350
228
229  Gly
230
231

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 1081

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105..1241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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252
253  CCTCGTGCCG GTCCTGAGGC CCTTCTCCAC CCGACAGAG TCCTTGGCCC ACCTCTCTCC      60
254
255  CACCCGACTC TGCCGAAAGA AGCACAGAAG CTCAAGCCGC CTCC ATG GCC CCA GGA      116
256      Met Ala Pro Gly
257      1
258

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text